

Kaufman

1646

#5
04/26/98

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/906,713

DATE: 04/10/98
TIME: 14:35:18

INPUT SET: S24888.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5 (i) APPLICANT: Lok, Si
6 Adams, Robyn L.
7 Jelmberg, Anna C.
8 Whitmore, Theodore E.
9 Farrah, Theresa M.
10
11 (ii) TITLE OF THE INVENTION: MAMMALIAN ZCYTOR11
12
13 (iii) NUMBER OF SEQUENCES: 6
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: ZymoGenetics
17 (B) STREET: 1201 Eastlake Ave East
18 (C) CITY: Seattle
19 (D) STATE: WA
20 (E) COUNTRY: USA
21 (F) ZIP: 98102
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Diskette
25 (B) COMPUTER: IBM Compatible
26 (C) OPERATING SYSTEM: DOS
27 (D) SOFTWARE: FastSEQ for Windows Version 2.0
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER:
36 (B) FILING DATE:
37
38
39
40 (viii) ATTORNEY/AGENT INFORMATION:
41 (A) NAME: Lunn, Paul G
42 (B) REGISTRATION NUMBER: 32,743
43 (C) REFERENCE/DOCKET NUMBER: 97-52
44
45
46 (ix) TELECOMMUNICATION INFORMATION:

INPUT SET: S24888.raw

47 (A) TELEPHONE: 206-442-6627
48 (B) TELEFAX: 206-442-6678
49 (C) TELEX:

50

51

52 (2) INFORMATION FOR SEQ ID NO:1:

53

54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 2831 base pairs
56 (B) TYPE: nucleic acid
57 (C) STRANDEDNESS: single
58 (D) TOPOLOGY: linear

59

60 (ii) MOLECULE TYPE: cDNA

61 (ix) FEATURE:

62

63 (A) NAME/KEY: Coding Sequence
64 (B) LOCATION: 34...1755
65 (D) OTHER INFORMATION:

66

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

68

69 TAGAGGCCAA	GGGAGGGCTC	TGTGCCAGCC	CCG	ATG	AGG	ACG	CTG	CTG	ACC	ATC	54					
70				Met	Arg	Thr	Leu	Leu	Thr	Ile						
71				1					5							
72																
73 TTG	ACT	GTG	GGA	TCC	CTG	GCT	CAC	GCC	CCT	GAG	GAC	CCC	TCG	GAT	102	
74 Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His	Ala	Pro	Glu	Asp	Pro	Ser	Asp	
75	10				15					20						
76																
77 CTG	CTC	CAG	CAC	GTG	AAA	TTC	CAG	TCC	AGC	AAC	TTT	GAA	AAC	ATC	CTG	150
78 Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	Ser	Asn	Phe	Glu	Asn	Ile	Leu	
79	25				30					35						
80																
81 ACG	TGG	GAC	AGC	GGG	CCA	GAG	GGC	ACC	CCA	GAC	ACG	GTC	TAC	AGC	ATC	198
82 Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	Pro	Asp	Thr	Val	Tyr	Ser	Ile	
83	40				45				50			55				
84																
85 GAG	TAT	AAG	ACG	TAC	GGA	GAG	AGG	GAC	TGG	GTG	GCA	AAG	AAG	GGC	TGT	246
86 Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	Trp	Val	Ala	Lys	Lys	Gly	Cys	
87	60				65				70							
88																
89 CAG	CGG	ATC	ACC	CGG	AAG	TCC	TGC	AAC	CTG	ACG	GTG	GAG	ACG	GGC	AAC	294
90 Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu	Thr	Val	Glu	Thr	Gly	Asn	
91	75				80				85							
92																
93 CTC	ACG	GAG	CTC	TAC	TAT	GCC	AGG	GTC	ACC	GCT	GTC	AGT	GGG	GGA	GGC	342
94 Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	
95	90				95				100							
96																
97 CGG	TCA	GCC	ACC	AAG	ATG	ACT	GAC	AGG	TTC	AGC	TCT	CTG	CAG	CAC	ACT	390
98 Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	
99	105				110				115							

INPUT SET: S24888.raw

100	ACC CTC AAG CCA CCT GAT GTG ACC TGT ATC TCC AAA GTG AGA TCG ATT	438
101	Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile	
102	120 125 130 135	
103		
104		
105	CAG ATG ATT GTT CAT CCT ACC CCC ACG CCA ATC CGT GCA GGC GAT GGC	486
106	Gln Met Ile Val His Pro Thr Pro Ile Arg Ala Gly Asp Gly	
107	140 145 150	
108		
109	CAC CGG CTA ACC CTG GAA GAC ATC TTC CAT GAC CTG TTC TAC CAC TTA	534
110	His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu	
111	155 160 165	
112		
113	GAG CTC CAG GTC AAC CGC ACC TAC CAA ATG CAC CTT GGA GGG AAG CAG	582
114	Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln	
115	170 175 180	
116		
117	AGA GAA TAT GAG TTC TTC GGC CTG ACC CCT GAC ACA GAG TTC CTT GGC	630
118	Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly	
119	185 190 195	
120		
121	ACC ATC ATG ATT TGC GTT CCC ACC TGG GCC AAG GAG AGT GCC CCC TAC	678
122	Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr	
123	200 205 210 215	
124		
125	ATG TGC CGA GTG AAG ACA CTG CCA GAC CGG ACA TGG ACC TAC TCC TTC	726
126	Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe	
127	220 225 230	
128		
129	TCC GGA GCC TTC CTG TTC TCC ATG GGC TTC CTC GTC GCA GTA CTC TGC	774
130	Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	
131	235 240 245	
132		
133		
134	TAC CTG AGC TAC AGA TAT GTC ACC AAG CCG CCT GCA CCT CCC AAC TCC	822
135	Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	
136	250 255 260	
137		
138	CTG AAC GTC CAG CGA GTC CTG ACT TTC CAG CCG CTG CGC TTC ATC CAG	870
139	Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	
140	265 270 275	
141		
142	GAG CAC GTC CTG ATC CCT GTC TTT GAC CTC AGC GGC CCC AGC AGT CTG	918
143	Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	
144	280 285 290 295	
145		
146	GCC CAG CCT GTC CAG TAC TCC CAG ATC AGG GTG TCT GGA CCC AGG GAG	966
147	Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	
148	300 305 310	
149		
150	CCC GCA GGA GCT CCA CAG CGG CAT AGC CTG TCC GAG ATC ACC TAC TTA	1014
151	Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	
152	315 320 325	

**RAW SEQUENCE LISTING
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INPUT SET: S24888.raw

153	GGG CAG CCA GAC ATC TCC ATC CTC CAG CCC TCC AAC GTG CCA CCT CCC	1062
154	Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
155	330 335 340	
156		
157		
158	CAG ATC CTC TCC CCA CTG TCC TAT GCC CCA AAC GCT GCC CCT GAG GTC	1110
159	Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
160	345 350 355	
161		
162	GGG CCC CCA TCC TAT GCA CCT CAG GTG ACC CCC GAA GCT CAA TTC CCA	1158
163	Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
164	360 365 370 375	
165		
166	TTC TAC GCC CCA CAG GCC ATC TCT AAG GTC CAG CCT TCC TCC TAT GCC	1206
167	Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
168	380 385 390	
169		
170	CCT CAA GCC ACT CCG GAC AGC TGG CCT CCC TCC TAT GGG GTA TGC ATG	1254
171	Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
172	395 400 405	
173		
174	GAA GGT TCT GGC AAA GAC TCC CCC ACT GGG ACA CTT TCT AGT CCT AAA	1302
175	Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys	
176	410 415 420	
177		
178		
179	CAC CTT AGG CCT AAA GGT CAG CTT CAG AAA GAG CCA CCA GCT GGA AGC	1350
180	His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	
181	425 430 435	
182		
183	TGC ATG TTA GGT GGC CTT TCT CTG CAG GAG GTG ACC TCC TTG GCT ATG	1398
184	Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
185	440 445 450 455	
186		
187	GAG GAA TCC CAA GAA GCA AAA TCA TTG CAC CAG CCC CTG GGG ATT TGC	1446
188	Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	
189	460 465 470	
190		
191	ACA GAC AGA ACA TCT GAC CCA AAT GTG CTA CAC AGT GGG GAG GAA GGG	1494
192	Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	
193	475 480 485	
194		
195	ACA CCA CAG TAC CTA AAG GGC CAG CTC CCC CTC CTC TCC TCA GTC CAG	1542
196	Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	
197	490 495 500	
198		
199	ATC GAG GGC CAC CCC ATG TCC CTC CCT TTG CAA CCT CCT TCC GGT CCA	1590
200	Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
201	505 510 515	
202		
203	TGT TCC CCC TCG GAC CAA GGT CCA AGT CCC TGG GGC CTG CTG GAG TCC	1638
204	Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	
205	520 525 530 535	

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/906,713DATE: 04/10/98
TIME: 14:35:21

INPUT SET: S24888.raw

206	CTT GTG TGT CCC AAG GAT GAA GCC AAG AGC CCA GCC CCT GAG ACC TCA	1686
207	Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser	
208	540	545
209		550
210		
211	GAC CTG GAG CAG CCC ACA GAA CTG GAT TCT CTT TTC AGA GGC CTG GCC	1734
212	Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala	
213	555	560
214		565
215	CTG ACT GTG CAG TGG GAG TCC TGAGGGAAAT GGGAAAGGCT TGGTGCTTCC TCCC	1789
216	Leu Thr Val Gln Trp Glu Ser	
217	570	
218		
219	TGTCCCTACC CAGTGTACAC TCCCTGGCTG TCAATCCCAT GCCTGCCCAT GCCACACACT	1849
220	CTGCGATCTG GCCTCAGACG GGTGCCCTTG AGAGAACAG AGGGAGTGGC ATGCAGGGCC	1909
221	CCTGCCATGG GTGCGCTCT CACCGGAACA AAGCAGCATG ATAAGGACTG CAGCGGGGGA	1969
222	GCTCTGGGA GCAGCTTGTG TAGACAAGCG CGTGCTCGCT GAGCCCTGCA AGGCAGAAAT	2029
223	GACAGTGCAC GGAGGAAATG CAGGGAAACT CCCGAGGTCC AGAGCCCCAC CTCCTAACAC	2089
224	CATGGATTCA AAGTGCTCAG GGAATTTGCC TCTCCTGCG CCATTCCCTGG CCAGTTTCAC	2149
225	AATCTAGCTC GACAGAGCAT GAGGCCCTG CCTCTTCTGT CATTGTTCAA AGGTGGGAAG	2209
226	AGAGCCTGGA AAAGAACAG GCCTGGAAAA GAACCAGAAG GAGGCTGGC AGAACACAGAA	2269
227	CAACCTGCAC TTCTGCCAAG GCCAGGGCCA GCAGGACGGC AGGACTCTAG GGAGGGGTGT	2329
228	GGCCTGCAGC TCATTCCAG CCAGGGCAAC TGCCTGACGT TGCACGATT CAGCTTCATT	2389
229	CCTCTGATAG AACAAAGCGA AATGCAGGTC CACCAGGGAG GGAGACACAC AAGCCTTTTC	2449
230	TGCAGGCAGG AGTTTCAGAC CCTATCCTGA GAATGGGGTT TGAAAGGAAG GTGAGGGCTG	2509
231	TGGCCCTGG ACGGGTACAA TAACACACTG TACTGATGTC ACAACTTTGC AAGCTCTGCC	2569
232	TTGGGTTTCAG CCCATCTGGG CTCAAATTCC ACCCTCACCA CTCACAAAGCT GTGTGACTTC	2629
233	AAACAAATGA AATCAGTGCC CAGAACCTCG GTTTCCTCAT CTGTAATGTG CGGATCATAA	2689
234	CACCTACCTC ATGGAGTTGT GGTGAAGATG AAATGAAGTC ATGTCTTTAA AGTGCCTTAAT	2749
235	AGTGCCTGGT ACATGGGCAG TGCCCAATAA ACGGTAGCTA TTTAAAAAAA AAAAAAAA	2809
236	AAAAAAATAG CGGCCGCCTC GA	2831
237		

238 (2) INFORMATION FOR SEQ ID NO:2:

239
 240 (i) SEQUENCE CHARACTERISTICS:
 241 (A) LENGTH: 574 amino acids
 242 (B) TYPE: amino acid
 243 (C) STRANDEDNESS: single
 244 (D) TOPOLOGY: linear
 245

246 (ii) MOLECULE TYPE: protein
 247 (v) FRAGMENT TYPE: internal
 248

249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

250
 251 Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 252 1 5 10 15
 253 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 254 20 25 30
 255 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 256 35 40 45
 257 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 258 50 55 60

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/906,713

DATE: 04/10/98
TIME: 14:35:22

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Line

Error

Original Text